

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/525,324A  
Source: Pt  
Date Processed by STIC: 1/27/06

# ***ENTERED***

## CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/525,324A

CRF Edit Date: 1/31/06  
Edited by: [signature]

\_\_\_ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

\_\_\_ Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

\_\_\_ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

\_\_\_ Deleted: \_\_\_ invalid beginning/end-of-file text ; \_\_\_ page numbers

\_\_\_ Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

\_\_\_ Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

✓  
\_\_\_ Other:  
Sequence 14 - used numeral "1" and numeral "0" in amino acid numbering (instead of letter "l" and letter "O")

Sequence 2 - replaced numeral "1" in "Artificial" with letter "l"

Revised 09/09/2003



PCT

## RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/525,324A

TIME: 14:48:13

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01312006\J525324A.raw

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3 <110> APPLICANT: SAKI, Mayumi
4     NONAKA, Hiromi
5     MIYAJI, Hiromasa
6     ICHIKAWA, Shunji
7     TAKASHIMA, Chiemi
8     MATSUMURA, Tsutomu
9     ARAI, Hitoshi
10    SASAKI, Katsutoshi
11    KOBATAKE, Choei
12    TSUKUMO, Yukihito
13    IIDA, Kyoichiro
14    KUBOYAMA, Takeshi
15    MANABE, Haruhiko
17 <120> TITLE OF INVENTION: Agent for prevention and/or treatment of itching
19 <130> FILE REFERENCE: 506.44793X00
21 <140> CURRENT APPLICATION NUMBER: US/10/525,324A
22 <141> CURRENT FILING DATE: 2005-02-22
24 <150> PRIOR APPLICATION NUMBER: JP 2002/241522
25 <151> PRIOR FILING DATE: 2002-08-22
27 <160> NUMBER OF SEQ ID NOS: 20
29 <170> SOFTWARE: PatentIn Ver 2.1
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32 <211> LENGTH: 54
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Synthetic DNA
39 <400> SEQUENCE: 1
40 tcgacaaata aagcaatagc atcacaaatt tcacaaataa agcatttttt tcaa 54
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 54
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Synthetic DNA
51 <400> SEQUENCE: 2
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54 <210> SEQ ID NO: 3
55 <211> LENGTH: 39
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic DNA

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Input Set : A:\PTO.AMC.txt

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62 <400> SEQUENCE: 3  
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66 <211> LENGTH: 39  
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68 <213> ORGANISM: Artificial Sequence  
70 <220> FEATURE:  
71 <223> OTHER INFORMATION: Synthetic DNA  
73 <400> SEQUENCE: 4  
74 gtacccccgg gctcgagttt ggacaaacca caactagaa 39  
76 <210> SEQ ID NO: 5  
77 <211> LENGTH: 40  
78 <212> TYPE: DNA  
79 <213> ORGANISM: Artificial Sequence  
81 <220> FEATURE:  
82 <223> OTHER INFORMATION: Synthetic DNA  
84 <400> SEQUENCE: 5  
85 tcgacggtat cgattcgact gacgtcatatc ttgacgtcac 40  
89 <210> SEQ ID NO: 6  
90 <211> LENGTH: 40  
91 <212> TYPE: DNA  
92 <213> ORGANISM: Artificial Sequence  
94 <220> FEATURE:  
95 <223> OTHER INFORMATION: Synthetic DNA  
97 <400> SEQUENCE: 6  
98 tcgagtgcgc tcaagtatga cgtcagtcga atcgataccg 40  
102 <210> SEQ ID NO: 7  
103 <211> LENGTH: 29  
104 <212> TYPE: DNA  
106 <213> ORGANISM: Artificial Sequence  
108 <220> FEATURE:  
109 <223> OTHER INFORMATION: Synthetic DNA  
111 <400> SEQUENCE: 7  
112 gccccagaag cttaagtgcc caccatggg 29  
116 <210> SEQ ID NO: 8  
117 <211> LENGTH: 33  
118 <212> TYPE: DNA  
119 <213> ORGANISM: Artificial Sequence  
121 <220> FEATURE:  
122 <223> OTHER INFORMATION: Synthetic DNA  
124 <400> SEQUENCE: 8  
125 gttcattgtg gcggccgcag catcttcagc tgc 33  
129 <210> SEQ ID NO: 9  
130 <211> LENGTH: 25  
131 <212> TYPE: DNA  
132 <213> ORGANISM: Artificial Sequence  
134 <220> FEATURE:  
135 <223> OTHER INFORMATION: Synthetic DNA  
137 <400> SEQUENCE: 9

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.AMC.txt

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145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
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153 <210> SEQ ID NO: 11
154 <211> LENGTH: 362
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 11
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160   1          5          10          15
162 His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu
163          20          25          30
165 Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln
166          35          40          45
168 Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu
169          50          55          60
171 Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His
172  65          70          75          80
174 Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile
175          85          90          95
177 Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser
178          100         105         110
180 Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu
181          115         120         125
183 Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr
184          130         135         140
186 Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg
187 145          150          155          160
189 Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly
190          165          170          175
192 Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe
193          180          185          190
195 Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val
196          195          200          205
198 Arg Gly Ser Val Ser Thr Gln Arg Gln Glu Lys Ala Lys Ile Lys Arg
199          210          215          220
201 Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr
202 225          230          235          240
204 His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp
205          245          250          255
207 Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu
208          260          265          270
210 Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu

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Input Set : A:\PTO.AMC.txt

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211          275          280          285
213 Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu
214          290          295          300
216 Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser
217 305          310          315          320
219 Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys
220          325          330          335
222 Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln
223          340          345          350
225 Val Gln Leu Lys Met Leu Pro Pro Ala Gln
226          355          360
228 <210> SEQ ID NO: 12
229 <211> LENGTH: 2932
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 12
234 ctgcagtcag gcggtgaact gacttcatcc caatccctca gccccaccca ggaccagtct 60
235 ggagtccttc cctgcccc attgaaattt cccttcgcgc cccaaactta cctctgatct 120
236 agaccttact cacctccttc ctgtttccta agactccttc ctgccgtcca cagaccgagc 180
237 cttttatctt tgtccaccct gtgccagaca cctccttttc cagaaccttc tccttactgg 240
238 tgaccttact tatctctgtt gctttctggg gtcctaggaa atgccagcac tcccaccac 300
239 attgcctgaa ctttccaaca ctccctagct gcgctgtgtc ctatctcaac acttccctcat 360
240 gtatttcttg tgtcttctag aacattcccc cgccattatt acttcaatat ggctacacat 420
241 acttccctaat tgccctgcaa accatctcct tctcaccatt gcccgatgat gctttcgtct 480
242 cctccataaa cactcccgga gaccaatttt tgtgtcacc ccatactccc tcgttgacac 540
243 actgactcca tacataacct ccttgaaaaa cctctttatt aatctcacca tcctccagac 600
244 ttcctcctcg tcataattcc atccctcctc caacttttcc ctctcaagct ctgcccttcc 660
245 cagcccagcc cagcctaccc aacctcatct ctccctgta gaccacatcc caccatgttc 720
246 cctgagcct ccaaggaagg ggctcagggg gcccctggc ctcccgtcc ctgtggcccc 780
247 acagcccccg tgggccaggg gaagcgcccc agaagccgaa gtgcccacc atg ggc aac 838
248                                     Met Gly Asn
249                                     1
251 cac acg tgg gag ggc tgc cac gtg gac tcg cgc gtg gac cac ctc ttt 886
252 His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp His Leu Phe
253          5          10          15
255 ccg cca tcc ctc tac atc ttt gtc atc ggc gtg ggg ctg ccc acc aac 934
256 Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu Pro Thr Asn
257 20          25          30          35
259 tgc ctg gct ctg tgg gcg gcc tac cgc cag gtg caa cag cgc aac gag 982
260 Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln Arg Asn Glu
261          40          45          50
263 ctg ggc gtc tac ctg atg aac ctc agc atc gcc gac ctg ctg tac atc 1030
264 Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu Leu Tyr Ile
265          55          60          65
267 tgc acg ctg ccg ctg tgg gtg gac tac ttc ctg cac cac gac aac tgg 1078
268 Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His Asp Asn Trp
269          70          75          80
271 atc cac ggc ccc ggg tcc tgc aag ctc ttt ggg ttc atc ttc tac acc 1126
272 Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile Phe Tyr Thr

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DATE: 01/31/2006

TIME: 14:48:13

Output Set: N:\CRF4\01312006\J525324A.raw

file:///C:/CRF4/OUTHOLD/VsrJ525324A.htm

VERIFICATION SUMMARY

DATE: 01/31/2006

PATENT APPLICATION: US/10/525,324A

TIME: 14:48:14

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01312006\J525324A.raw



**Raw Sequence Listing before editing  
(for reference only)**



PCT

## RAW SEQUENCE LISTING

DATE: 01/27/2006

PATENT APPLICATION: US/10/525,324A

TIME: 09:50:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01272006\J525324A.raw

3 <110> APPLICANT: SAKI, Mayumi  
 4 NONAKA, Hiromi  
 5 MIYAJI, Hiromasa  
 6 ICHIKAWA, Shunji  
 7 TAKASHIMA, Chiemi  
 8 MATSUMURA, Tsutomu  
 9 ARAI, Hitoshi  
 10 SASAKI, Katsutoshi  
 11 KOBATAKE, Choei  
 12 TSUKUMO, Yukihiro  
 13 IIDA, Kyoichiro  
 14 KUBOYAMA, Takeshi  
 15 MANABE, Haruhiko  
 17 <120> TITLE OF INVENTION: Agent for prevention and/or treatment of itching  
 19 <130> FILE REFERENCE: 506.44793X00  
 21 <140> CURRENT APPLICATION NUMBER: US/10/525,324A  
 22 <141> CURRENT FILING DATE: 2005-02-22  
 24 <150> PRIOR APPLICATION NUMBER: JP 2002/241522  
 25 <151> PRIOR FILING DATE: 2002-08-22  
 27 <160> NUMBER OF SEQ ID NOS: 20  
 29 <170> SOFTWARE: PatentIn Ver 2.1

## ERRORED SEQUENCES

438 <210> SEQ ID NO: 14  
 439 <211> LENGTH: 1098  
 440 <212> TYPE: DNA  
 441 <213> ORGANISM: Mus musculus  
 443 <400> SEQUENCE: 14  
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 445 Met Asp Asn Ser Thr Gly Thr Gly Glu Gly Cys His Val Asp Ser Arg  
 446 1 5 10 15  
 448 gtg gac cac ctc ttc cca cca tct ctc tac atc ttc gtc atc ggg gtg 96  
 449 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
 450 20 25 30  
 452 ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgg cag gtg 144  
 453 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
 454 35 40 45  
 456 cgc caa cac aat gag ctg ggc gtc tac ctg atg aac ttg agc att gca 192  
 457 Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
 458 50 55 60  
 460 gac ctg ctg tac atc tgc act ttg ccg ctg tgg gtc gac tac ttc ctc 240

Does Not Comply  
 Corrected Diskette Needed

P.2

## RAW SEQUENCE LISTING

DATE: 01/27/2006

PATENT APPLICATION: US/10/525,324A

TIME: 09:50:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01272006\J525324A.raw

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461 Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu
462 65 70 75 80
464 cac cat gac aac tgg atc cac ggc cct ggc tcc tgc aag ctc ttt ggc 288
465 His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly
466 85 90 95
468 ttc atc ttc tac agc aac atc tat atc agc atc gcc ttc ctg tgc tgc 336
469 Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys
470 100 105 110
472 atc tcc gtg gac cgc tac ctg gct gtg gct cat cct ctg cgc ttt gca 384
473 Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala
474 115 120 125
476 cgc ctg cgc cgg gtc aag aca gca gtg gct gtg agc tct gtg gtc tgg 432
477 Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp
478 130 135 140
480 gcc acg gag ctg ggc gcc aat tca gca ccg ctc ttc cat gat gag ctg 480
481 Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu
E--> 482 145 150 155 use number 1 ← 0600 ← use number "φ"
E--> 484 ttt cgt gat cgc tac aac cac acc ttc tgc ttt gag aag ttc ccc atg 528
485 Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met
W--> 486 165 170 175
E--> 488 gag cgt tgg gtg gcc tgg atg aat ctg tac cgc gtc ttt gtg ggc ttc 576
489 Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe
490 180 185 190
E--> 492 ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgt ggc atc ctg agg 624
493 Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg
494 195 200 205
E--> 496 gca gtg cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc 672
497 Ala Val Gln Ser Ser Val Ser Thr Glu Arg Glu Glu Lys Val Lys Ile
498 210 215 220
E--> 500 aaa cgt ctg gcc ctg agc ctc atc gcc att gtg ctg gtg tgc ttt gcg 720
501 Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala
502 225 230 235 240
E--> 504 cct tac cat gct ctc ctg ctg tct cgc agc gcc gtc tac ctg ggc cgg 768
505 Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg
506 245 250 255
E--> 508 ccc tgg gac tgt ggc ttc gag gag cga gtc ttt tct gcc tac cac agc 816
509 Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser
510 260 265 270
E--> 512 tcc ctg gcc ttc acc agc ctc aat tgt gtg gct gac ccc atc ctc tac 864
513 Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr
514 275 280 285
E--> 516 tgc ctg gtc aac gag ggt gcc cgc agt gat gtg gcc aag gcc ctg cac 912
517 Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His
518 290 295 300
E--> 520 aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat 960
521 Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn
522 305 310 315 320
E--> 524 gct tcc ctc acc ctg gag aca ccc ttg acc tcc aag agg agc acc acc 1008
525 Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr

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Input Set : A:\PTO.RJ.txt

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526 325 330 335  
 E--> 528 ggc aag tcg tcc ggg gct gtc tgg gca gtg cct ccg act gcc cag ggg 1056  
 529 Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
 530 340 345 350  
 E--> 532 gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga 1098  
 533 Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
 E--> 534 355 360 365  
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 638 <211> LENGTH: 1098  
 639 <212> TYPE: DNA  
 E--> 640 <213> Rattus norvegicus  
 E--> 642  
 642 <400> SEQUENCE: 18  
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 645 1 5 10 15  
 647 gtg gac cac ctc ttc cca cca tcc ctc tac atc ttc gtc atc ggg gtg 96  
 648 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
 649 20 25 30  
 651 ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgc cag gtg 144  
 652 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
 653 35 40 45  
 655 cgc cag cgc aat gag ctg ggc gtc tac ctg atg aac ttg agc atc gca 192  
 656 Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
 657 50 55 60  
 659 gac ctg ctg tac atc tgt acg ctg ccg ctg tgg gtc gac tac ttc ctc 240  
 660 Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu  
 661 65 70 75 80  
 663 cac cat gac aac tgg atc cac ggc ccc ggc tcc tgc aag ctc ttt ggc 288  
 664 His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly  
 665 85 90 95  
 667 ttc atc ttc tac agc aac atc tac atc agc atc gcc ttc ctg tgc tgc 336  
 668 Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys  
 669 100 105 110  
 671 atc tcc gtg gac cgc tac ctg gct gtg gcc cat ccg ctg cgc ttt gcg 384  
 672 Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala  
 673 115 120 125  
 675 cgc ctg cgc cgg gtc aag aca gca gta gct gtg agc tcc gtg gtc tgg 432  
 676 Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp  
 677 130 135 140  
 679 gcc acc gag cta ggc gcc aac tcg gca ccg ctc ttt cat gac gag ctc 480  
 680 Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu  
 681 145 150 155 160  
 683 ttt cgt gat cgc tac aac cac acc ttc tgc ttc gag aag ttc ccc atg 528  
 684 Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met  
 685 165 170 175  
 687 gag cgc tgg gtg gcc tgg atg aac ctg tac cgc gtc ttt gtg ggg ttc 576  
 688 Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe  
 689 180 185 190

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Input Set : A:\PTO.RJ.txt

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691	ctc	ttc	ccc	tgg	gca	ctc	atg	ttg	ctg	tgc	tac	cgc	ggc	atc	ctg	cgg	624
692	Leu	Phe	Pro	Trp	Ala	Leu	Met	Leu	Leu	Cys	Tyr	Arg	Gly	Ile	Leu	Arg	
693			195					200					205				
695	gcc	gta	cag	agc	agt	gtg	tcc	acc	gag	cgc	cag	gag	aaa	gtc	aag	atc	672
696	Ala	Val	Gln	Ser	Ser	Val	Ser	Thr	Glu	Arg	Gln	Glu	Lys	Val	Lys	Ile	
697		210					215					220					
699	aaa	cgc	ctg	gcc	ctg	agc	ctc	atc	gcc	atc	gtg	ctg	gtg	tgc	ttt	gca	720
700	Lys	Arg	Leu	Ala	Leu	Ser	Leu	Ile	Ala	Ile	Val	Leu	Val	Cys	Phe	Ala	
701	225						230				235					240	
703	ccc	tac	cat	gct	ctc	ttg	ctg	tct	cgc	agc	gct	gtc	tat	ctg	ggc	cgg	768
704	Pro	Tyr	His	Ala	Leu	Leu	Leu	Ser	Arg	Ser	Ala	Val	Tyr	Leu	Gly	Arg	
705					245					250					255		
707	ccc	tgg	gac	tgt	ggc	ttc	gag	gag	cga	gtc	ttc	tct	gcc	tac	cac	agc	816
708	Pro	Trp	Asp	Cys	Gly	Phe	Glu	Glu	Arg	Val	Phe	Ser	Ala	Tyr	His	Ser	
709			260						265				270				
711	tcc	cta	gcc	ttc	acc	agc	ctc	aat	tgc	gtg	gct	gac	ccc	atc	ctc	tac	864
712	Ser	Leu	Ala	Phe	Thr	Ser	Leu	Asn	Cys	Val	Ala	Asp	Pro	Ile	Leu	Tyr	
713		275						280				285					
715	tgc	ctg	gtc	aac	gag	ggg	gcc	cgt	agt	gac	gtg	gcc	aaa	gcc	ctg	cac	912
716	Cys	Leu	Val	Asn	Glu	Gly	Ala	Arg	Ser	Asp	Val	Ala	Lys	Ala	Leu	His	
717		290					295				300						
719	aac	ctc	ctc	cgc	ttc	ctg	gcc	agc	aac	aag	ccc	cag	gag	atg	gcc	aat	960
720	Asn	Leu	Leu	Arg	Phe	Leu	Ala	Ser	Asn	Lys	Pro	Gln	Glu	Met	Ala	Asn	
721	305					310				315					320		
723	gct	tcc	ctc	acc	ctg	gag	aca	cca	ttg	acc	tcc	aag	agg	agc	acc	acc	1008
724	Ala	Ser	Leu	Thr	Leu	Glu	Thr	Pro	Leu	Thr	Ser	Lys	Arg	Ser	Thr	Thr	
725				325					330					335			
727	ggc	aaa	acg	tct	ggg	gct	gtc	tgg	gca	gtg	cct	ccc	act	gcc	cag	ggg	1056
728	Gly	Lys	Thr	Ser	Gly	Ala	Val	Trp	Ala	Val	Pro	Pro	Thr	Ala	Gln	Gly	
729			340					345				350					
731	gac	cag	gtg	cca	ctg	aag	gtg	ctg	ctg	ccc	ccg	gca	cag	tga			1098
732	Asp	Gln	Val	Pro	Leu	Lys	Val	Leu	Leu	Pro	Pro	Ala	Gln				
733			355				360					365					

## VERIFICATION SUMMARY

DATE: 01/27/2006

PATENT APPLICATION: US/10/525,324A

TIME: 09:50:50

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01272006\J525324A.raw

L:46 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14  
L:482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:482 SEQ:14  
L:482 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12  
L:484 M:254 E: No. of Bases conflict, LENGTH:Input:528 Counted:530 SEQ:14  
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14  
L:488 M:254 E: No. of Bases conflict, LENGTH:Input:576 Counted:578 SEQ:14  
L:492 M:254 E: No. of Bases conflict, LENGTH:Input:624 Counted:626 SEQ:14  
L:496 M:254 E: No. of Bases conflict, LENGTH:Input:672 Counted:674 SEQ:14  
L:500 M:254 E: No. of Bases conflict, LENGTH:Input:720 Counted:722 SEQ:14  
L:504 M:254 E: No. of Bases conflict, LENGTH:Input:768 Counted:770 SEQ:14  
L:508 M:254 E: No. of Bases conflict, LENGTH:Input:816 Counted:818 SEQ:14  
L:512 M:254 E: No. of Bases conflict, LENGTH:Input:864 Counted:866 SEQ:14  
L:516 M:254 E: No. of Bases conflict, LENGTH:Input:912 Counted:914 SEQ:14  
L:520 M:254 E: No. of Bases conflict, LENGTH:Input:960 Counted:962 SEQ:14  
L:524 M:254 E: No. of Bases conflict, LENGTH:Input:1008 Counted:1010 SEQ:14  
L:528 M:254 E: No. of Bases conflict, LENGTH:Input:1056 Counted:1058 SEQ:14  
L:532 M:254 E: No. of Bases conflict, LENGTH:Input:1098 Counted:1100 SEQ:14  
L:534 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1098 Found:1100 SEQ:14  
L:640 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:642 M:282 E: Numeric Field Identifier Missing, <213> is required.